Mapping QTLs for Resistance to Root Rots Caused by *Phytophthora tropicalis* in Cassava

**J. B. Loke**1, E. Alvarez1, M. Fregene1, J. Marin1, S. Rivera2, G. A. Llano1, and J. F. Mejia1

1Centro Internacional de Agricultura Tropical (CIAT); 2Universidad del Valle, Cali, Colombia

### Introduction

Several species of *Phytophthora* (Loke 2004) attack cassava (*Manihot esculenta* Crantz), causing severe root rot and wilting (Figure 1). The development of *Phytophthora* is favored by inadequate agronomic conditions, inoculating shoots and roots with species that were previously identified by sequencing the internal transcribed spacer region in rDNA.

### Materials and Methods

**Plant materials.** We harvested and evaluated 1-year-old roots belonging to the cassava K family (92 individuals, years 2000 and 2001, Santander de Quilichao, Cauca, Colombia) and CM 9582 (43 genotypes, year 2001, Florida, Valle, Colombia) in 2000 and 2001. One resistant (M Bra 1045) and one susceptible (M Col 2066) variety to root rot were also included as checks.

**Molecular techniques.** We clonally propagated the female-derived cassava map (K family) and used molecular markers based on microsatellites, expressed sequence tags (ESTs) and known genes. The detection of false positives, a significant association between a DNA marker and *Phytophthora* resistance was declared if the probability was more than 0.005. The degree of phenotypic variance explained by each marker was obtained from the regression coefficient ($r^2$). All data were analyzed with Q-gene software on McIntosh.

### Results and Discussion

Genotypes of the cassava K family, evaluated during 2000 and 2001, showed infected areas covering between 22% and 80% of roots (Figure 2). The distribution of frequencies of root area affected by *P. tropicalis* corresponded to a normal distribution.

Some genotypes that had, in 2000, intermediate resistance to *P. tropicalis* tended to become susceptible in 2001 and vice versa (Figure 3). The correlation between the evaluations of 2000 and 2001 was -0.15.

Genotypes of the cassava family CM 9582 (M Bra 1045 × M CR 81) showed 70% to 90% of areas infected. The distribution of frequency of CM 9582 genotypes for area infected by *P. tropicalis* presented a rising curve. As shown in previous studies, M Bra 1045 is tolerant of *P. tropicalis*. The genetic base of M Bra 1045 can be assumed to be polygenic, and to have epitasis in this cross.

### Conclusions

Results show that resistance to *Phytophthora* root rot is polygenic in the cassava K family. The occurrence of individuals more resistant than the two parents and the detection of QTLs associated with molecular markers from the female-derived map show that resistance alleles coming from both parents contribute to resistance in the progenies (transgressive segregation). Such characteristics are well known in heterozygous species and are useful for combining resistance genetic factors in the same cultivar (Jorge et al. 2001).

Although the populations differed in their genetic base of resistance to *Phytophthora*, the levels of resistance observed were not sufficiently high to warrant use in genetic improvement programs. Hence, identifying new parents and developing new populations are desirable.

### References


Jorge V; Fregene M; Velez CM; Duque MC; Tohme J; Verdier V. 2001. QTL analysis of field resistance to Xanthomonas axonopodis pv. manihotis in cassava. Theor Appl Genet 102:564-571.